

## Comments / Suggestions

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Result No.	Score	% Query Match	Length	DB	ID	Description
1	4824	100.0	991	3	AAY83171	Aay83171 Cell wall
2	4824	100.0	991	3	AAY70120	Aay70120 Staph. ep
3	4820	99.9	930	5	ABP40469	Abp40469 Staphyloc
4	4820	99.9	930	8	ADS06014	Ads06014 Staphyloc
5	4640	96.2	892	8	ADO84849	Ado84849 S epiderm
6	4640	96.2	892	8	ADS20651	Ads20651 S. epider
7	4638	96.1	892	6	ABU42557	Abu42557 Protein e
8	4485	93.0	1092	2	AAW41602	Aaw41602 Staphyloc
9	4485	93.0	1092	7	ABM79019	Abm79019 Staphyloc
10	2814	58.3	560	7	ABM79015	Abm79015 Staphyloc
11	2616.5	54.2	549	7	ABM79020	Abm79020 Staphyloc
12	2442	50.6	670	6	ABU42520	Abu42520 Protein e
13	2132	44.2	1166	2	AAY08643	Aay08643 S. aureus
14	2131	44.2	1166	6	ABJ18982	Abj18982 Pathogen
15	2127.5	44.1	1141	6	ABU42327	Abu42327 Protein e
16	1725	35.8	331	9	AEB23146	Aeb23146 Ligand bi
17	1695	35.1	343	7	ABM79016	Abm79016 Staphyloc
18	1585	32.9	316	7	ABM79017	Abm79017 Staphyloc
19	1544.5	32.0	1633	6	ABU42513	Abu42513 Protein e
20	1543.5	32.0	1802	3	AAY83170	Aay83170 Cell wall
21	1543.5	32.0	1802	3	AAY70119	Aay70119 Staph. ep
22	1500.5	31.1	1315	2	AAY08642	Aay08642 S. aureus
23	1500.5	31.1	1315	6	ABJ18969	Abj18969 Pathogen
24	1485.5	30.8	1349	4	AAU37544	Aau37544 Staphyloc
25	1485.5	30.8	1349	4	AAU34402	Aau34402 Staphyloc
26	1485.5	30.8	1349	6	ABM72436	Abm72436 Staphyloc
27	1463.5	30.3	841	4	AAU37158	Aau37158 Staphyloc
28	1463.5	30.3	841	4	AAU34283	Aau34283 Staphyloc
29	1459.5	30.3	953	6	ABU16533	Abu16533 Protein e
30	1446.5	30.0	1385	6	ABU16400	Abu16400 Protein e
31	1428	29.6	932	4	AAU36845	Aau36845 Staphyloc
32	1428	29.6	932	4	AAU34082	Aau34082 Staphyloc
33	1427.5	29.6	947	6	ABJ18940	Abj18940 Pathogen
34	1424	29.5	1920	6	ABU43489	Abu43489 Protein e
35	1404.5	29.1	995	6	ABM72437	Abm72437 Staphyloc
36	1398.5	29.0	930	2	AAY08641	Aay08641 S. aureus
37	1376	28.5	1155	4	AAG82343	Aag82343 S. epider
38	1069.5	22.2	278	4	AAG82803	Aag82803 S. epider
39	962	19.9	287	4	AAG81687	Aag81687 S. epider
40	891.5	18.5	936	2	AAW89801	Aaw89801 Staphyloc
41	884	18.3	877	6	ABU42504	Abu42504 Protein e
42	884	18.3	933	6	ABJ18947	Abj18947 Pathogen
43	883	18.3	927	6	ABM72221	Abm72221 Staphyloc
44	881	18.3	877	6	ADA89539	Ada89539 Staphyloc
45	881	18.3	877	6	ABM72702	Abm72702 Staphyloc

## ALIGNMENTS

## RESULT 1

AAY83171

ID AAY83171 standard; protein; 991 AA.

XX

AC AAY83171;

XX

DT 24-JUL-2000 (first entry)

XX  
DE Cell wall protein SdrG.  
XX  
KW SdrF; SdrG; SdrH; coagulase negative; staphylococcus; septicemia;  
KW osteomyelitis; endocarditis; immune response; vaccine; graft; stent;  
KW intravenous catheter; heart valve; cardiac.  
XX  
OS Staphylococcus sp.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 14  
FT /note= "Position encoded by TAG stop codon"  
FT Misc-difference 33  
FT /note= "Position encoded by TGA stop codon"  
FT Misc-difference 964  
FT /note= "Position encoded by TAA stop codon"  
FT Misc-difference 980  
FT /note= "Position encoded by TAG stop codon"  
FT Misc-difference 989  
FT /note= "Position encoded by TAA stop codon"  
XX  
PN WO200012689-A1.  
XX  
PD 09-MAR-2000.  
XX  
PF 31-AUG-1999; 99WO-US019728.  
XX  
PR 31-AUG-1998; 98US-0098443P.  
PR 25-JAN-1999; 99US-0117119P.  
XX  
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
XX  
PI Foster TJ, Hook M, Davis S, Hartford O, Mccrea K, Ni Eidhin D;  
XX  
DR WPI; 2000-256637/22.  
DR N-PSDB; AAZ93534.  
XX  
PT Recombinant or synthetic proteins from coagulase-negative staphylococci  
PT useful for prevention, treatment and diagnosis of staphylococcal  
PT infections bind soluble and immobilized fibrinogen.  
XX  
PS Claim 8; Fig 3; 104pp; English.  
XX  
CC Isolated Staphylococcus Sdr cell wall proteins which bind both soluble  
CC and immobilized fibrinogen are useful for treating or preventing  
CC coagulase-negative staphylococcal infection such as septicemia,  
CC osteomyelitis or endocarditis, and for inducing immune responses in  
CC patients. The cell wall proteins are also useful for reducing coagulase-  
CC negative staphylococci infection of indwelling medical devices such as  
CC vascular grafts, vascular stents, intravenous catheters, artificial heart  
CC valves and cardiac assist devices. The cell wall associated proteins are  
CC able to inhibit staphylococcal adhesion to immobilised extracellular  
CC matrix or host cells present on the surface of implanted biomaterials  
XX  
SQ Sequence 991 AA;

Query Match 100.0%; Score 4824; DB 3; Length 991;  
Best Local Similarity 100.0%; Pred. No. 1.2e-229;  
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LKKNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	60
Db	34	LKKNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	93
Qy	61	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Db	94	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	153
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	180
Db	154	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	213
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Db	214	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	273
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Db	274	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	333
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	334	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	393
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	394	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	453
Qy	421	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Db	454	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	513
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Db	514	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	573
Qy	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Db	574	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	633
Qy	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEEGKYQFDGLKNGLTY	660
Db	634	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEEGKYQFDGLKNGLTY	693
Qy	661	KITFETPEGYTPTLKHSGTNPALDSEGNSVWVTINGQDDMTIDSGFYQTPKYSLGNYVWY	720
Db	694	KITFETPEGYTPTLKHSGTNPALDSEGNSVWVTINGQDDMTIDSGFYQTPKYSLGNYVWY	753
Qy	721	DTNKDGIQGDDDEKGISGVKVTCLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	780
Db	754	DTNKDGIQGDDDEKGISGVKVTCLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	813
Qy	781	MTQTTTDSGDDDEQDADGEEVHVTTITDHDDFSIDNGYYDDSDSDSDSDSDSDSDSDSDSD	840
Db	814	MTQTTTDSGDDDEQDADGEEVHVTTITDHDDFSIDNGYYDDSDSDSDSDSDSDSDSDSDSD	873
Qy	841	SDSGLDNSSDKNTKDKLPDTGANEDH	900
Db	874	SDSGLDNSSDKNTKDKLPDTGANEDH	933
Qy	901	DSKGTLLGALFAGLGALLLGKRRKNRKNKN	930

|||||  
 Db 934 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 963

## RESULT 2

AAY70120

ID AAY70120 standard; protein; 991 AA.

XX

AC AAY70120;

XX

DT 06-JUN-2000 (first entry)

XX

DE Staph. epidermidis serine-aspartate repeat region protein SdrG.

XX

KW Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;  
 KW microbial surface components recognising adhesive matrix molecules;  
 KW collagen binding protein; CBP; CNA; fibrinogen binding protein;  
 KW Clumping factor A; ClfA; Clumping factor B; ClfB; FnBP;  
 KW fibronectin binding protein; Staphylococcus infection;  
 KW serine-aspartate repeat region protein; SDR protein; SdrG.

XX

OS Staphylococcus epidermidis.

XX

FH Key Location/Qualifiers

FT Misc-difference 14

FT /note= "Encoded by in-frame stop codon TAG"

FT Misc-difference 33

FT /note= "Encoded by in-frame stop codon TGA"

FT Misc-difference 964

FT /note= "Encoded by in-frame stop codon TAA"

FT Misc-difference 980

FT /note= "Encoded by in-frame stop codon TAG"

FT Misc-difference 989

FT /note= "Encoded by in-frame stop codon TAA"

XX

PN WO200012131-A1.

XX

PD 09-MAR-2000.

XX

PF 31-AUG-1999; 99WO-US019727.

XX

PR 31-AUG-1998; 98US-0098439P.

XX

PA (INHI-) INHIBITEX INC.

PA (TEXA ) UNIV TEXAS A &amp; M SYSTEM.

PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.

XX

PI Patti JM, Foster TJ, Hook M;

XX

DR WPI; 2000-237781/20.

DR N-PSDB; AAZ51202.

XX

PT Composition used for generating immune response or for inhibiting  
 PT microbial colonization in an animal comprises antibodies that bind  
 PT collagen binding protein, fibrinogen binding protein and, optionally,  
 PT fibronectin binding protein.

XX

PS Claim 8; Fig 4; 115pp; English.

XX

CC The patent discloses multicomponent vaccines containing selected  
 CC combinations of bacterial binding proteins termed MSCRAMM (microbial

CC surface components recognising adhesive matrix molecules) or their  
 CC antibodies. A vaccine composition is provided that includes collagen  
 CC binding protein or peptide, e.g. CNA, a fibrinogen binding protein  
 CC preferably Clumping factor A (ClfA) or Clumping factor B (ClfB), and  
 CC optionally a fibronectin binding protein e.g. FnBP-A. The vaccines are  
 CC useful for imparting protection against a broad spectrum of  
 CC Staphylococcal strains and for inhibiting microbial colonisation,  
 CC especially of Staphylococcus aureus, in an animal. The combinations can  
 CC also be used to select donor blood pools for the preparation of purified  
 CC blood products for passive immunisation. The present sequence is a serine  
 CC -aspartate repeat region protein, SdrG from Staphylococcus epidermidis.  
 CC The Sdr protein is useful in vaccine preparation in combination with  
 CC specific bacterial binding proteins. These vaccines can be used to treat  
 CC a broad spectrum of bacterial infections, including those arising from  
 CC both coagulase-positive and coagulase-negative bacteria

XX

SQ Sequence 991 AA;

Query Match 100.0%; Score 4824; DB 3; Length 991;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-229;  
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	60
Db	34	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	93
Qy	61	NMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Db	94	NMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	153
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	180
Db	154	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	213
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Db	214	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	273
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Db	274	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	333
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	334	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	393
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	394	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	453
Qy	421	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Db	454	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	513
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Db	514	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	573
Qy	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQDLPPEKTYK	600
Db	574	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQDLPPEKTYK	633

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Qy      601 IGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGT SKSVRTDEEGKYQFDGLKNGLT Y 660
      |||||||
Db      634 IGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGT SKSVRTDEEGKYQFDGLKNGLT Y 693

Qy      661 KITFETPEGYTPTLK HSGTNPALDSEGNSVWVTINGQDDMTIDSGFYQTPKYS LGNYVWY 720
      |||||||
Db      694 KITFETPEGYTPTLK HSGTNPALDSEGNSVWVTINGQDDMTIDSGFYQTPKYS LGNYVWY 753

Qy      721 DTNKDGIQGDDDEKGISGVKVT LKDENGNIISTTTT DENGKYQFDNLNSGNYIVHFDKPSG 780
      |||||||
Db      754 DTNKDGIQGDDDEKGISGVKVT LKDENGNIISTTTT DENGKYQFDNLNSGNYIVHFDKPSG 813

Qy      781 MTQTTTDSGDDDEQDADGEEVHV TITDHDDFSIDNGYYDDSDSDSDSDSDSDSDSDSDSD 840
      |||||||
Db      814 MTQTTTDSGDDDEQDADGEEVHV TITDHDDFSIDNGYYDDSDSDSDSDSDSDSDSDSDSD 873

Qy      841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 900
      |||||||
Db      874 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 933

Qy      901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930
      |||||||
Db      934 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 963

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## RESULT 3

ABP40469

ID ABP40469 standard; protein; 930 AA.

XX

AC ABP40469;

XX

DT 24-JUL-2002 (first entry)

XX

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.

XX

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
KW antibacterial; gene therapy.

XX

OS Staphylococcus epidermidis.

XX

PN US6380370-B1.

XX

PD 30-APR-2002.

XX

PF 13-AUG-1998; 98US-00134001.

XX

PR 14-AUG-1997; 97US-0055779P.

PR 08-NOV-1997; 97US-0064964P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucette-Stamm LA, Bush D;

XX

DR WPI; 2002-381255/41..

DR N-PSDB; ABN93014.

XX

PT Novel isolated nucleic acid encoding a Staphylococcus epidermis

PT polypeptide, useful for diagnosing and treating bacterial infections.

XX

PS Disclosure; SEQ ID NO 5314; 267pp; English.

XX

CC ABN90538 to ABN93374 represent *Staphylococcus epidermidis* open reading  
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 CC given in ABP35124 to ABP37960. The *S. epidermidis* sequences have  
 CC antibacterial activity and can be used in gene therapy. The sequences can  
 CC also be used in the diagnosis and treatment of bacterial infections,  
 CC particularly *S. epidermidis* infections. The sequences can be used to  
 CC screen for compounds able to interfere with the *S. epidermidis* life cycle  
 CC or inhibit *S. epidermidis* infection. N.B. The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 99.9%; Score 4820; DB 5; Length 930;  
 Best Local Similarity 99.9%; Pred. No. 1.7e-229;  
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	60
Db	1	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGATLLFGLGHNEAKAEENTVQDVKDS	60
Qy	61	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Db	61	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVSESSSSMDTAQQPSHTTINSEASIQTSDNE	180
Db	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVSESSSSMDTAQQPSHTTINSEASIQTSDNE	180
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Db	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Db	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Qy	421	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Db	421	VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Db	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Qy	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Db	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Qy	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLTY	660
Db	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLTY	660



[illegible]

## RESULT 4

ADS06014

ID ADS06014 standard; protein; 930 AA.

XX

AC      ADS06014;

XX

DT 04-NOV-2004 (first entry)

XX

DE Staphylococcus epidermis polypeptide seqid 5309.

XX

KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;

KW recombinant expression vector; infection; computer readable medium;

KW computer based system.

XX

OS     Staphylococcus epidermidis.

XX

PN US2004147734-A1.

XX

PD 29-JUL-2004.

XX

PF 01-DEC-2003; 2003US-00724972.

XX

PR 08-NOV-1997; 97US-0064964P.

PR 13-AUG-1998; 98US-00134001.

PR 29-NOV-1999; 99US-00450969.

XX

PA (DOUC/) DOUCETTE-STAMM L.

PA (BUSH/) BUSH D.

XX

PI Doucette-Stamm L, Bush D:

XX

DR WPI; 2004-580138/56.

DR N-PSDB; ADS02242.

XX

PT New isolated polypeptide and encoding nucleic acid derived from

PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or

PT     treating an *S. epidermidis* bacterial infection.

XX

PS Claim 17; SEQ ID NO 5309; 741pp; English.

XX

CC The invention describes an isolated nucleic acid comprising a nucleotide  
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
 CC given in the specification. Also described are: a recombinant expression  
 CC vector; a cell comprising a recombinant expression vector of (1);  
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection, comprising a nucleic acid cited above and a carrier; treating  
 CC a subject for S. epidermidis infection; a recombinant or substantially  
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
 CC sample; a computer readable medium having recorded in it the nucleotide  
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
 CC system for identifying fragments of the Staphylococcus genome of  
 CC commercial importance; a computer based system for identifying fragments  
 CC of the Staphylococcus plasmids of commercial importance; identifying  
 CC commercially important nucleic acid fragments of the Staphylococcus  
 CC genome and/or plasmids; and identifying an expression modulating fragment  
 CC of the Staphylococcus genome and/or plasmids. The methods and  
 CC compositions of the present invention are useful for the diagnosis,  
 CC prevention and/or treatment of an Staphylococcal epidermidis bacterial  
 CC infection. This is the amino acid sequence of a S. epidermis protein of  
 CC the invention.

XX

SQ Sequence 930 AA;

Query Match 99.9%; Score 4820; DB 8; Length 930;  
 Best Local Similarity 99.9%; Pred. No. 1.7e-229;  
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS	60
Db	1	LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGATLLFGLGHNEAKAEENTVQDVKDS	60
Qy	61	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Db	61	NMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN	120
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	180
Db	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	180
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Db	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Db	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420

Qy	421	VEYQKPENERTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Db	421	VEYQKPENERTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKV	540
Db	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKV	540
Qy	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Db	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Qy	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLT	660
Db	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLT	660
Qy	661	KITFETPEGYTPTLKHSCTNPALDSEGNVSVVVTINGQDDMTIDSGFYQTPKYSLGNYVWY	720
Db	661	KITFETPEGYTPTLKHSCTNPALDSEGNVSVVVTINGQDDMTIDSGFYQTPKYSLGNYVWY	720
Qy	721	DTNKDGIQGDDEKGISGVKVLTKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	780
Db	721	DTNKDGIQGDDEKGISGVKVLTKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	780
Qy	781	MTQTTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGGYDDSDSDSDSDSDSDSDSDSDSD	840
Db	781	MTQTTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGGYDDSDSDSDSDSDSDSDSDSDSD	840
Qy	841	SDSGLDNSSDKNTKDKLPDTGANEDH	900
Db	841	SDSGLDNSSDKNTKDKLPDTGANEDH	900
Qy	901	DSKGTLLGALFAGLGALLGKRRKRNKKN	930
Db	901	DSKGTLLGALFAGLGALLGKRRKRNKKN	930

## RESULT 5

ADO84849

ID AD084849 standard; protein; 892 AA.

XX

AC ADO84849:

XX

DT 29-JUL-2004 (first entry)

XX

DE S epidermidis surface anchored LPXTG protein SeqID21.

XX

KW LPXTG; cell wall-anchored surface protein; Gram positive bacterium;

KW extracellular matrix molecule; sequence database; C-terminal;

KW Immunoglobulin-like fold region; Ig-like fold region; antibacterial;

KW vaccine; gene therapy; infection; medical device; prosthesis;

KW premature newborn; AIDS; debilitated cancer; bone marrow transplantation.

XX

OS    Staphylococcus epidermidis.

XX

PN WO2004025416-A2.

XX

PD 25-MAR-2004.

XX

PF 15-SEP-2003; 2003WO-US028789.

XX  
 PR 13-SEP-2002; 2002US-0410303P.  
 XX  
 PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
 PA (INHI-) INHIBITEX INC.  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Hook M, Xu Y, Sillanpaa JV, Sthanam N, Ponnuraj K, Patti JM;  
 PI Hutchins JT, Hall A;  
 XX  
 DR WPI; 2004-315684/29.  
 XX  
 PT Identifying LPXTG-containing cell wall-anchored surface proteins from  
 PT Gram positive bacteria, for treating infection caused by the bacteria,  
 PT comprises searching sequence information database for the sequence having  
 PT LPXTG-motif.  
 XX  
 PS Claim 16; SEQ ID NO 21; 96pp; English.  
 XX  
 CC This invention relates to a novel method of identifying LPXTG-containing  
 CC cell wall-anchored surface proteins from Gram positive bacteria that bind  
 CC to an extracellular matrix molecule which comprises searching a database  
 CC of sequence information for a putative protein sequence having the LPXTG-  
 CC motif in its C-terminal region and analysing the sequence for the  
 CC presence of one or more Immunoglobulin (Ig)-like fold regions. The  
 CC invention may be useful for the production of compounds with an  
 CC antibacterial activity or for production of a vaccine. In addition the  
 CC disclosed sequences may be useful for gene therapy. The antibody is  
 CC useful for treating or preventing an infection of Gram-positive bacteria  
 CC in a human or animal patient. The method and the proteins are useful in  
 CC generating antibodies for treating and preventing the spread of  
 CC infections of Gram positive bacteria, for interfering with, or inhibiting  
 CC binding interactions by Gram positive bacteria, for monitoring the level  
 CC of gram positive bacterial antigens, or antibodies recognising the  
 CC antigens in a human or animal patients suspected of containing the  
 CC antigens or antibodies, in preventing or reducing infection of medical  
 CC devices and prosthesis caused by such organisms, and in treating or  
 CC preventing infections in highly susceptible groups such as premature  
 CC newborns, AIDS and debilitated cancer patients, and bone marrow  
 CC transplantation. The present sequence is that of a surface anchored LPXTG  
 CC protein identified using the method of the invention.  
 XX  
 SQ Sequence 892 AA;

Query Match 96.2%; Score 4640; DB 8; Length 892;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-220;  
 Matches 892; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 LFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK 98  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 LFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK 60  
 Qy 99 EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD 158  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD 120  
 Qy 159 TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSI 218  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSI 180  
 Qy 219 TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV 278

Db	181	TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV	240
Qy	279	NHLIKVTDQSITEGYDDSDGIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	338
Db	241	NHLIKVTDQSITEGYDDSDGIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	300
Qy	339	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	398
Db	301	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	360
Qy	399	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	458
Db	361	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	420
Qy	459	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYQA	518
Db	421	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYQA	480
Qy	519	LGNNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGFEFRTASYDN	578
Db	481	LGNNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGFEFRTASYDN	540
Qy	579	TIAFSTSSGQGQDLPPEKTYKIGDYVWEDVDKDGIONTNDNEKPLSNVLVLTLYPDGTS	638
Db	541	TIAFSTSSGQGQDLPPEKTYKIGDYVWEDVDKDGIONTNDNEKPLSNVLVLTLYPDGTS	600
Qy	639	KSVRTDEEGKYQFDGLKNGLTYSKITFETPEGYTPTLKHSGTNPALDSEGNVSVWVTINGQD	698
Db	601	KSVRTDEEGKYQFDGLKNGLTYSKITFETPEGYTPTLKHSGTNPALDSEGNVSVWVTINGQD	660
Qy	699	DMTIDSGFYQTPKYSLGNYVWYDTNKGDIQGDDEKGISGVKVTCLKDENGNIISTTTTIDEN	758
Db	661	DMTIDSGFYQTPKYSLGNYVWYDTNKGDIQGDDEKGISGVKVTCLKDENGNIISTTTTIDEN	720
Qy	759	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	818
Db	721	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	780
Qy	819	DDSG	878
Db	781	DDSG	840
Qy	879	LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLLGKRRKNRKNKN	930
Db	841	LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLLGKRRKNRKNKN	892

## RESULT 6

ADS20651

ID ADS20651 standard; protein; 892 AA.

XX

AC ADS20651;

XX

DT 30-DEC-2004 (first entry)

XX

DE S. epidermidis hyperimmune serum reactive antigen protein - SEQ ID 52..

XX

KW antigen; antibiotic resistance; antibacterial; vaccine; gene therapy.

XX

OS Staphylococcus epidermidis.

XX  
 PN WO2004087746-A2.  
 XX  
 PD 14-OCT-2004.  
 XX  
 PF 31-MAR-2004; 2004WO-EP003398.  
 XX  
 PR 31-MAR-2003; 2003EP-00450078.  
 XX  
 PA (INTE-) INTERCELL AG.  
 XX  
 PI Meinke A, Min Bui D, Nagy E;  
 XX  
 DR WPI; 2004-729219/71.  
 DR N-PSDB; ADS20620.  
 XX  
 PT New nucleic acid molecules encoding hyperimmune serum reactive antigens  
 PT from Staphylococcus epidermidis, useful for diagnosing, preventing or  
 PT treating S. epidermidis infections.  
 XX  
 PS Claim 11; SEQ ID NO 52; 196pp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid molecule encoding  
 CC a hyperimmune serum reactive antigen or its fragment. Staphylococci are  
 CC commonly associated with human disease. Both Staphylococcus epidermidis  
 CC and Staphylococcus aureus have become resistant to many commonly used  
 CC antibiotics, most importantly methicillin (MRSA) and vancomycin (VISA).  
 CC Drug resistance is an increasingly important public health concern and  
 CC novel therapies to combat staphylococci infection must be developed in  
 CC preparation for a time when such infections may be untreatable by  
 CC antibiotics. The molecules of the invention demonstrate antibacterial  
 CC activity and may be useful for manufacturing a medicament, such as a  
 CC vaccine, for treating or preventing S. epidermidis infections, possibly  
 CC via gene therapy. The antigen or its fragment may also be used for  
 CC generating an anticaline peptide binding to the hyperimmune serum  
 CC reactive antigen or fragment, for manufacturing a functional nucleic  
 CC acid, such as an aptamer or spiegelmer and for manufacturing a functional  
 CC ribonucleic acid, such as a ribozyme, antisense nucleic acid or siRNA  
 CC (short interfering RNA). The current sequence is that of a Staphylococcus  
 CC epidermidis hyperimmune serum reactive antigen protein of the invention.  
 XX  
 SQ Sequence 892 AA;

Query Match 96.2%; Score 4640; DB 8; Length 892;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-220;  
 Matches 892; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 LFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK 98  
 |||  
 Db 1 LFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK 60  
 Qy 99 EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD 158  
 |||  
 Db 61 EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD 120  
 Qy 159 TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSI 218  
 |||  
 Db 121 TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSI 180  
 Qy 219 TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV 278  
 |||

Db	181	TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV	240
Qy	279	NHLIKVTDQSITEGYDDSDGIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	338
Db	241	NHLIKVTDQSITEGYDDSDGIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	300
Qy	339	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	398
Db	301	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	360
Qy	399	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	458
Db	361	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	420
Qy	459	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQ	518
Db	421	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQ	480
Qy	519	LGNNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDN	578
Db	481	LGNNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDN	540
Qy	579	TIAFSTSSGQGQGDLPPEKTYKIGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGTS	638
Db	541	TIAFSTSSGQGQGDLPPEKTYKIGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGTS	600
Qy	639	KSVRTDEEGKYQFDGLKNGLT YKITFETPEGYTPTLKHSGTNPALDSEGN SVWVTINGQD	698
Db	601	KSVRTDEEGKYQFDGLKNGLT YKITFETPEGYTPTLKHSGTNPALDSEGN SVWVTINGQD	660
Qy	699	DMTIDSGFYQTPKYSLGNYVWYDTNKGDIQG DDEKGISGVKVT LKDENGNIISTTTT DEN	758
Db	661	DMTIDSGFYQTPKYSLGNYVWYDTNKGDIQG DDEKGISGVKVT LKDENGNIISTTTT DEN	720
Qy	759	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	818
Db	721	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	780
Qy	819	DDSG	878
Db	781	DDSG	840
Qy	879	LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLLGKRRKNRKNKN	930
Db	841	LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLLGKRRKNRKNKN	892

## RESULT 7

ABU42557

ID ABU42557 standard; protein; 892 AA.

XX

AC ABU42557;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #28084.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Staphylococcus epidermidis.

XX

PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA46427.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 70481; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 892 AA;

Query Match 96.1%; Score 4638; DB 6; Length 892;



Best Local Similarity 99.9%; Pred. No. 1.5e-220;  
Matches 891; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	39	LFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK	98
		:	
Db	1	MFGLGHNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKK	60
Qy	99	EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD	158
Db	61	EETNSNDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMD	120
Qy	159	TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVRRED SI	218
Db	121	TAQQPSHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVRRED SI	180
Qy	219	TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV	278
Db	181	TSQPSSYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNV	240
Qy	279	NHLIKVTDQSITEGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	338
Db	241	NHLIKVTDQSITEGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSD	300
Qy	339	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	398
Db	301	LTDSFAIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVP	360
Qy	399	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	458
Db	361	NNNTKLDVEYKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLR	420
Qy	459	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDY AQ	518
Db	421	YSAKETNVNISGNGDEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDY AQ	480
Qy	519	LGNNDNVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGFEFTASYDN	578
Db	481	LGNNDNVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGFEFTASYDN	540
Qy	579	TIAFSTSSGQGQGLPPEKTYKIGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGTS	638
Db	541	TIAFSTSSGQGQGLPPEKTYKIGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTYPDGTS	600
Qy	639	KSVRTDEEGKYQFDGLKNGLT YKITFETPEGYTPTLKHSGTNPALDSEGNSVWVTINGQD	698
Db	601	KSVRTDEEGKYQFDGLKNGLT YKITFETPEGYTPTLKHSGTNPALDSEGNSVWVTINGQD	660
Qy	699	DMTIDSGFYQTPKYSLGNYVWYDTNKDGIQGDDDEKGISGVKVT LKDENGNIISTTTT DEN	758
Db	661	DMTIDSGFYQTPKYSLGNYVWYDTNKDGIQGDDDEKGISGVKVT LKDENGNIISTTTT DEN	720
Qy	759	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	818
Db	721	GKYQFDNLNSGNYIVHFDKPSGMTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYY	780
Qy	819	DDSG	878
Db	781	DDSG	840
Qy	879	LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLGKRRKNRKNKN	930

Db 841 LDNSSDKNTKDKLPDTGANEDHDSKGTLLGALFAGLGALLLGKRRKRNKKN 892

## RESULT 8

AAW41602

ID AAW41602 standard; protein; 1092 AA.

XX

AC AAW41602;

XX

DT 17-OCT-2003 (revised)

DT 22-JUN-1998 (first entry)

XX

DE Staphylococcus epidermidis fibrinogen binding protein FIG.

XX

KW Fibrinogen binding protein; FIG; aggregation; infection;

KW coagulase-negative Staphylococcus; therapy; diagnosis; immunisation;

KW immunogen; vaccine.

XX

OS Staphylococcus epidermidis; strain HB.

XX

FH Key Location/Qualifiers

FT Peptide 1. .51

FT /label= Sig\_peptide

FT Protein 52. .1092

FT /label= Mat\_protein

FT Region 52. .824

FT /note= "non-repetitive region, harbours fibrinogen binding activity"

FT Region 825. .1040

FT /note= "Asp-Ser dipeptide repeat region"

FT Region 1053. .1057

FT /note= "cell wall anchoring motif"

XX

PN WO9748727-A1.

XX

PD 24-DEC-1997.

XX

PF 18-JUN-1997; 97WO-SE001091.

XX

PR 20-JUN-1996; 96SE-00002496.

XX

PA (GUSS/) GUSS B.

PA (NILS/) NILSSON M.

PA (FRYK/) FRYKBERG L.

PA (FLOC/) FLOCK J.

PA (LIND/) LINDBERG M.

XX

PI Guss B, Nilsson M, Frykberg L, Flock J, Lindberg M;

XX

DR WPI; 1998-063079/06.

DR N-PSDB; AAV04279.

XX

PT Fibrinogen-binding protein from coagulase-negative Staphylococcus - used for prevention, treatment and diagnosis of Staphylococcus infection.

XX

PS Example 3; Fig 6; 45pp; English.

XX

CC The protein comprises the fibrinogen binding protein (FIG) of coagulase-negative Staphylococcus epidermidis HB. Its amino acid sequence was deduced from the isolated fig gene (see AAV04279). The closest known analogue of FIG is the clumping factor of S. aureus which also binds

CC fibrinogen and promotes bacterial aggregation in serum. Recombinant FIG  
CC polypeptides can be expressed in host cells. They are used as immunogens,  
CC particularly in vaccines (which may be expressed in vivo) to protect  
CC humans and animals against coagulase-negative Staphylococcus infection.  
CC Antibodies raised against FIG can be used for passive immunisation. They  
CC block the adherence of bacteria) and for diagnosis. (Updated on 17-OCT-  
CC 2003 to standardise OS field)

XX

SQ Sequence 1092 AA;

Query Match 93.0%; Score 4485; DB 2; Length 1092;  
Best Local Similarity 81.1%; Pred. No. 7e-213;  
Matches 883; Conservative 19; Mismatches 27; Indels 160; Gaps 3;

Qy	2	KKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDSN	61
Db	4	KKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGATLLFGLGHNEAKAEENSVQDVKDSN	63
Qy	62	MDELSDSNDQSSNEEKNDVINNSQSINTDDDNQ- IKKEETNSNDAIENRSKDITQSTTN	120
Db	64	TDELSDSNDQSSDEEKNDVINNNQSINTDDNNQIIKKEETNNYDGIEKRSEDRTSTTN	123
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE	180
Db	124	VDENEATFLQKTPQDNTHLTEEEVKESSVESSNSSIDTAQQPSHTTINREESVQTSNDV	183
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
Db	184	EDSHVSDFANSKIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELLN	243
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
Db	244	LPINEYENKARPLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGI	303
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	304	KAHDAENLIYDVTFEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNSGEIIATGT	363
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	364	YDNKNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	423
Qy	421	VEYQKPENERTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
Db	424	VEYQRPENERTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	483
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Db	484	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	543
Qy	541	ISKYDPNKDDYTTIIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Db	544	ISKYDPNKDDYTTIIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	603
Qy	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEEGKYQFDGLKNGLTY	660
Db	604	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEDGKYQFDGLKNGLTY	663
Qy	661	KITFETPEGYTPTLKHSHTNPALDSEGNVSVVVTINGQDDMTIDSGFYQTPKYSLGNYVWY	720
Db	664	KITFETPEGYTPTLKHSHTNPALDSEGNVSVVVTINGQDDMTIDSGFYQTPKYSLGNYVWY	723

Qy	721	DTNKDGIQGDDDEKGISGVKVTCLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	780
Db	724	DTNKDGIQGDDDEKGISGVKVTCLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG	783
Qy	781	MTQTTTTDSGDDDEQDADGEEVHVITIDHDDFSIDNGYYDDSDSDSDSDSDSDSD-----	833
Db	784	MTQTTTTDSGDDDEQDADGEEVHVITIDHDDFSIDNGYYDDES DSDSDSDSDSDSDSDSDSDSDS	843
Qy	834	-----	833
Db	844	DS	903
Qy	834	-----	833
Db	904	DS	963
Qy	834	DSGLD-----	880
Db	964	DSVSDSDSDSDSDS	1023
Qy	881	-----NSSDKNTKD KLPDTGANEDHDSKGTLLGALFAGLGALLLGK	921
Db	1024	GSDSDSDSDSDSDNDSDLGNSSDKSTKD KLPDTGANEDYGSKGTLLGTLFAGLGALLLGK	1083
Qy	922	RRKNRKNKN	930
Db	1084	RRKNRKNKN	1092

## RESULT 9

ABM79019

ID ABM79019 standard; protein; 1092 AA.

XX

AC ABM79019;

XX

DT 15-JAN-2004 (first entry)

XX

DE Staphylococcus epidermidis polypeptide.

XX

KW Infection; antibacterial; vaccine.

XX

OS Staphylococcus epidermidis.

XX

PN WO2003076470-A1.

XX

PD 18-SEP-2003.

XX

PF 05-MAR-2003; 2003WO-US006415.

XX

PR 05-MAR-2002; 2002US-0361324P.

XX

PA (INHI-) INHIBITEX INC.

PA (TEXA ) UNIV TEXAS A & M SYSTEM.

XX

PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;

PI Robbins J, Vernachio J, Bowden MG;

XX

DR WPI; 2003-722324/68.

XX

PT New antibody recognizing a Staphylococcus epidermidis protein comprising

PT SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for  
PT treating or preventing a coagulase-negative Staphylococcal infection.  
XX  
PS Claim 16; Page 36-37; 78pp; English.  
XX  
CC The present sequence comprises the protein sequence of a polypeptide of a  
CC coagulase-negative Staphylococcus epidermidis. A claimed monoclonal  
CC antibody recognises this protein and is used in a claimed method of  
CC treating or preventing a coagulase-negative staphylococcal infection in a  
CC human or animal, e.g. a nosocomial coagulase-negative staphylococcal  
CC infection in low birth weight infants  
XX  
SQ Sequence 1092 AA;

Query Match 93.0%; Score 4485; DB 7; Length 1092;  
Best Local Similarity 81.1%; Pred. No. 7e-213;  
Matches 883; Conservative 19; Mismatches 27; Indels 160; Gaps 3;

Qy	2	KKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDSN	61
Db	4	KKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGATLLFGLGHNEAKAEENSVDVQDVKDSN	63
Qy	62	MDELSDSNDQSSNEEKNDVINNSQSINTDDDNQ-IKKEETNSNDAIENRSKDITQSTTN	120
		:     :     :     :     :     :     :     :	
Db	64	TDDELSDSNDQSSDEEKNDVINNNQSINTDDNNQIIKKEETNNYDGIEKRSEDRTESTTN	123
Qy	121	VDENEATFLQKTPQDNTQLKEEVVKEPSSVSESSSSMDTAQQPSHTTINSEASIQTSDNE	180
		:     :     :     :     :     :     :     :	
Db	124	VDENEATFLQKTPQDNTHLTEEEVKESSSVSESSSSIDTAQQPSHTTINREESVQTSNDV	183
Qy	181	ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN	240
		:                         :	
Db	184	EDSHVSDFANSKIKESNTESGKEENTIEQPNKVREDSTTSQPSGYTNIDEKISNQDELLN	243
Qy	241	LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII	300
		:	
Db	244	LPINEYENKARPLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGI	303
Qy	301	KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT	360
Db	304	KAHDAENLIYDVTFEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNSGEIIATGT	363
Qy	361	YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	420
Db	364	YDNKNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT	423
Qy	421	VEYQKPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	480
		:	
Db	424	VEYQRPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID	483
Qy	481	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	540
Db	484	DSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV	543
Qy	541	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	600
Db	544	ISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGLPPEKTYK	603
Qy	601	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSSKSVRTDEEGKYQFDGLKNGLTY	660
Db	604	IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTPDGTSSKSVRTDEDGKYQFDGLKNGLTY	663

[illegible]

RESULT 10

ABM79015

ID    ABM79015 standard; protein; 560 AA.

XX

AC ABM79015;

XX

DT 15-JAN-2004 (first entry)

XX

DE Staphylococcus epidermidis SdrG N1N2N3 domain.

XX

KW SdrG; surface protein; infection; antibacterial; vaccine.

XX

OS    Staphylococcus epidermidis.

XX

PN WO2003076470-A1.

XX

PD 18-SEP-2003.

XX

PF 05-MAR-2003; 2003WO-US006415.

XX

PR 05-MAR-2002; 2002US-0361324P.

XX

PA (INHI-) INHIBITEX INC.

PA (TEXA ) UNIV TEXAS A & M SYSTEM.

XX

PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;

PI Robbins J, Vernachio J, Bowden MG;

XX  
 DR WPI; 2003-722324/68.  
 DR N-PSDB; ACF80624.  
 XX  
 PT New antibody recognizing a Staphylococcus epidermidis protein comprising  
 PT SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for  
 PT treating or preventing a coagulase-negative Staphylococcal infection.  
 XX  
 PS Claim 27; Page 24-25; 78pp; English.  
 XX  
 CC The present sequence comprises the protein sequence of the N1N2N3 region  
 CC (amino acids 50-597), or putative A domain, of the SdrG surface protein  
 CC of coagulase-negative Staphylococcus epidermidis. A claimed antibody  
 CC recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The  
 CC antibody may be a monoclonal antibody, including a chimeric, murine,  
 CC humanized, human or single chain monoclonal antibody, which prevents a  
 CC coagulase-negative staphylococcal infection in a human or animal by  
 CC inhibiting binding of staphylococcus bacteria to fibrinogen. Such  
 CC antibodies can be used to treat or prevent staphylococcal infections  
 CC including nosocomial coagulase-negative staphylococcal infections in low  
 CC birth weight infants. A claimed vaccine comprises the isolated SdrG  
 CC N1N2N3, N2N3 or TR2 protein  
 XX  
 SQ Sequence 560 AA;

Query Match 58.3%; Score 2814; DB 7; Length 560;  
 Best Local Similarity 99.1%; Pred. No. 8.8e-131;  
 Matches 549; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	44	HNEAKAEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNS	103
		: :	
Db	7	HHHHGSEENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNS	66
Qy	104	NDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQP	163
Db	67	NDAIENRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQP	126
Qy	164	SHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPS	223
Db	127	SHTTINSEASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPS	186
Qy	224	SYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIK	283
Db	187	SYKNIDEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIK	246
Qy	284	VTDQSITGEYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSF	343
Db	247	VTDQSITGEYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSF	306
Qy	344	AIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTK	403
Db	307	AIPKIKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTK	366
Qy	404	LDVEYKTALSSVNKTITVEYQKPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKE	463
Db	367	LDVEYKTALSSVNKTITVEYQKPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKE	426
Qy	464	TNVNISGNGDEGSTIIDDSTIIKVYKVGDNQNLPSNRIDYSEYEDVTNDDYAQLGNNN	523
Db	427	TNVNISGNGDEGSTIIDDSTIIKVYKVGDNQNLPSNRIDYSEYEDVTNDDYAQLGNNN	486

```

Qy      524 DVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFS 583
          |||
Db      487 DVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTIAFS 546

Qy      584 TSSGQGQGDLPPEK 597
          |||
Db      547 TSSGQGQGDLPPEK 560

```

## RESULT 11

ABM79020

ID ABM79020 standard; protein; 549 AA.

XX

AC ABM79020;

XX

DT 15-JAN-2004 (first entry)

XX

DE Staphylococcus epidermidis polypeptide.

XX

KW Infection; antibacterial; vaccine.

XX

OS Staphylococcus epidermidis.

XX

PN WO2003076470-A1.

XX

PD 18-SEP-2003.

XX

PF 05-MAR-2003; 2003WO-US006415.

XX

PR 05-MAR-2002; 2002US-0361324P.

XX

PA (INHI-) INHIBITEX INC.

PA (TEXA ) UNIV TEXAS A &amp; M SYSTEM.

XX

PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;

PI Robbins J, Vernachio J, Bowden MG;

XX

DR WPI; 2003-722324/68.

XX

PT New antibody recognizing a Staphylococcus epidermidis protein comprising

PT SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for

PT treating or preventing a coagulase-negative Staphylococcal infection.

XX

PS Claim 20; Page 37; 78pp; English.

XX

CC The present sequence comprises the protein sequence of a polypeptide of a

CC coagulase-negative Staphylococcus epidermidis. A claimed monoclonal

CC antibody recognises this protein and is used in a claimed method of

CC treating or preventing a coagulase-negative staphylococcal infection in a

CC human or animal, e.g. a nosocomial coagulase-negative staphylococcal

CC infection in low birth weight infants

XX

SQ Sequence 549 AA;

Query Match 54.2%; Score 2616.5; DB 7; Length 549;

Best Local Similarity 92.7%; Pred. No. 4.8e-121;

Matches 509; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

```

Qy      50 EENTVQDVKDSNMDELSDSNDQSSNEEKNDVINNSQSINTDDDNQI-KKEETNSNDAIE 108
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
Db      1 EENSVQDVKDSNTDELSDSNDQSSDEEENDVINNNQSINSDDNNQINKKEETNNNDGIE 60

```



Qy	109	NRSKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVNESSMDTAQQPSHTTI	168
Db	61	KSSEDRTESTTNVDENEATFLQKSPQDNTHLTEEEVKEPSSVNESSSIDTAQQPSHTTI	120
Qy	169	NSEASIQTS DNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNI	228
Db	121	NREESVQTS DNVEDSHVSDFANSKIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNI	180
Qy	229	DEKISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQS	288
Db	181	DEKISNQDELLNLPINEYENKARPLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQS	240
Qy	289	ITEGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKI	348
Db	241	ITEGYDDSEGVIIKAHDAENLIYDVTFEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKI	300
Qy	349	KDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEY	408
Db	301	KDNSGEIIATGTYDNKNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEY	360
Qy	409	KTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNI	468
Db	361	KTALSSVNKTITVEYQRPENENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNI	420
Qy	469	SGNGDEGSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNIN	528
Db	421	SGNGDEGSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNIN	480
Qy	529	FGNIDSPYIIKVISKYDPNKDDYTTIQQTVTMQTTINEYTGFEFTASYDNTIAFSTSSGQ	588
Db	481	FGNIDSPYIIKVISKYDPNKDDYTTIQQTVTMQTTINEYTGFEFTASYDNTIAFSTSSGQ	540
Qy	589	GQGDLPPEK 597	
Db	541	GQGDLPPEK 549	

## RESULT 12

ABU42520

ID    ABU42520 standard; protein; 670 AA.

XX

AC ABU42520;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #28047.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS    Staphylococcus epidermidis.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA46390.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 70444; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 670 AA;

Query Match 50.6%; Score 2442; DB 6; Length 670;  
 Best Local Similarity 71.8%; Pred. No. 2.5e-112;  
 Matches 483; Conservative 4; Mismatches 4; Indels 182; Gaps 3;

Qy 437 MFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIIDDSTIIKVYKVGDNQNL 496  
 |||  
 Db 1 MFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIIDDSTIIKVYKVGDNQNL 60  
 Qy 497 PDSNRIYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQ 556  
 |||

[illegible]

RESULT 13

AAV08643

ID AAY08643 standard; protein; 1166 AA.

XX

AC AAY08643;

XX

DT 20-MAR-2003 (revised)

DT 09-AUG-1999 (first entry)

XX

DE S. aureus SdrE protein.

XX

KW Fibrinogen-binding protein; alpha chain; beta chain; ClfB; SdrC; SdrD;  
KW SdrE; fibrinogen; medical device; competitive inhibitor; pharmaceutical;  
KW treatment; infection; septicemia; osteomyelitis; mastitis; endocarditis;  
KW extracellular matrix; vascular graft; vascular stent; vaccine;  
KW intravenous catheter; artificial heart valve; cardiac assist device;  
KW antibacterial.  
XX

OS Staphylococcus aureus.  
 XX  
 PN WO9927109-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 25-NOV-1998; 98WO-US025246.  
 XX  
 PR 26-NOV-1997; 97US-0066815P.  
 PR 31-AUG-1998; 98US-0098427P.  
 XX  
 PA (INHI-) INHIBITEX INC.  
 PA (FORF-) FORFAS T/A BIORESEARCH IRELAND.  
 PA (TEXA ) UNIV TEXAS A & M.  
 PA (PATT/) PATTI J M.  
 PA (FOST/) FOSTER T J.  
 PA (JOSE/) JOSEFSSON E.  
 PA (EIDH/) EIDHIN D N.  
 PA (HOOK/) HOOK M A O.  
 PA (PERK/) PERKINS S E.  
 XX  
 PI Patti JM, Foster TJ, Josefsson E, Eidhin DN, Hook MAO;  
 PI Perkins SE;  
 XX  
 DR WPI; 1999-357844/30.  
 DR N-PSDB; AAX77594.  
 XX  
 PT Staphylococcus aureus fibrinogen-binding proteins for treating  
 PT septicemia, osteomyelitis, mastitis or endocarditis.  
 XX  
 PS Claim 8; Fig 9; 143pp; English.  
 XX  
 CC This invention describes novel Staphylococcus aureus fibrinogen-binding  
 CC proteins that bind both the alpha and beta fibrinogen chains. The  
 CC proteins (and their encoding nucleic acids are ClfB, SdrC, SdrD and  
 CC SdrE). Staphylococcus aureus is thought to utilize fibrinogen to adhere  
 CC to medical devices, binding proteins that bind both the alpha and beta  
 CC fibrinogen chains (ClfB, SdrC, SdrD and SdrE) can therefore be used as  
 CC competitive inhibitors to block this binding. Antibodies against ClfB,  
 CC SdrC, SdrD and SdrE inhibit ClfB, SdrC, SdrD and SdrE mediated binding.  
 CC The proteins of the invention can be used in a pharmaceutical composition  
 CC for the treatment of Staphylococcus aureus infection e.g. septicemia,  
 CC osteomyelitis, mastitis or endocarditis or to inhibit the binding of S.  
 CC aureus to the extracellular matrix. The proteins or their fragments may  
 CC be used to coat a medical device to reduce the S. aureus infection of an  
 CC indwelling medical device, especially where the medical device is  
 CC selected from the group consisting of vascular grafts, vascular stents,  
 CC intravenous catheters, artificial heart valves, and cardiac assist  
 CC devices. ClfB, SdrC, SdrD, SdrE, or an active fragment, subdomain or  
 CC encoding gene may be used as a vaccine. The DS (aspartate serine) repeat  
 CC region or a gene encoding it may be used as an identifying probe for the  
 CC identification of genes and encoding proteins from Staphylococcus aureus  
 CC (other than ClfA), S. hemolyticus, S. lugdenensis, and S. schleriferi.  
 CC The proteins of the invention have antibacterial activity. (Updated on 20  
 CC -MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 1166 AA;

Query Match 44.2%; Score 2132; DB 2; Length 1166;  
 Best Local Similarity 40.8%; Pred. No. 1e-96;  
 Matches 482; Conservative 149; Mismatches 265; Indels 286; Gaps 25;

Qy	7	LTXXXPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDSNMDEL	66
		:     : :   ::   :       ::   :   :         ::	
Db	10	ITKGMISNRLNKFIRKYTVGTASILVGTTLIFGLGNQEAKAAENT--STENAKQDDAT	67
Qy	67	SDSNDQ--SSNEEKNDVINNS-----QSINTDDDNQIKKEETNSNDAIENRSKDITQST-	118
		:   :     :     :     :      :  : : : :  :	
Db	68	TSNDKEVVSETENNSTTENNSTNPIKKETNTDSQPEAKKESTSS--STQKQNNVTATTE	125
Qy	119	---TNVD-ENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASI	174
		::       :  :    :: : : : :  :  : : :	
Db	126	TKPQNIKENVKPSTDKTATEDTSVILEEKKAPNNTNNDVTTPKSTSEPSTSEIQTKPTT	185
Qy	175	-QTSNDNEENS RVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKIS	233
		:   :  : : :    : : :     :	
Db	186	PQESTNIENSQPQP-TPSKVDNQVTDATNP----KEPVNVSKEELKNNPEKLKELVRNDS	240
Qy	234	NQDELLNLPINEYENKVRPLSTTSAQPSSKRV-----TVNQLAAEQGSNVNHLIKVTDQ	287
		: :  :           :	
Db	241	NTD-----HSTKPVATAPTSVAPKRVNAKMRFAVAQPAVASNNVNDLIKVTQ	289
Qy	288	SITEGYDDSDGIKAHAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPK	347
		:      :     ::      : :        :      :	
Db	290	TIKVG-DGKDNVAAAHDGKDIEYDTEFTIDNKVKKGDGMTINYDKNVIPSDLTDKNPID	348
Qy	348	IKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVE	407
		:     :             :                   ::	
Db	349	ITDPSGEVIAKGTFDKATKQITYTFTDYVDKYEDIKSRLTLYSYIDKKTVP-NETSLNLT	407
Qy	408	YKTALSSVNKTITVEYQKPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVN	467
		:    : : : :    : : : :    :      : :          :	
Db	408	FATAGKETSQNVTVDYQDPMVHGDSNIQSIFTKLDEDKQTIEQQIYVNPLKKSATNTKVD	467
Qy	468	ISGNG-----DEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTND-DYA	517
		: :       :        :           : :        :	
Db	468	IAGSQVDDYGNIKLGNGSTIIDQNTIEIKVYKVNSDQQLPQSNRIYDFSQYEDVTSQFDNK	527
Qy	518	QLGNNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYD	577
		: :  :  : : :        :          :  :  :  :  :  :	
Db	528	KSFSNNVATLDFGDINSAYIIKVVS KYTPTS DGELDIAQGTSMRTT-DKY-GYNYAGYS	585
Qy	578	NTIAFSTSSGQGGDL-PPEKTYKIGDYVWEDVDKGIQNTNDNEKPLSNVLVTLTYPDG	636
		:      :                  :    :    :	
Db	586	NFIVTSNDTGGDGTVKPEEKLYKIGDYVWEDVDKGVQGTDSKEKPMANVLVTLTYPDG	645
Qy	637	TSKSVRTDEEGKYQFDGLKNGLT YKITFETPEGYTPTLKHSGTNPALDSEGNSVWVTING	696
		:           :     :      :            :   :     :	
Db	646	TTKSVRTDANGHYEFGGLKDGETYTVKFETPTGYLP TKVNGTTDGEKDSNGSSVTVKING	705
Qy	697	QDDMTIDSGFYQTPKYS LGNYVWYDTNKGDIQGDDEKGISGVKVT LKDENGNIISTTT--	754
		:   : : :      : : :          :              :	
Db	706	KDDMSLDTG FYKEPKYN LGDYVWEDTNKGDIQDANEPGIKDVKVT LKDSTGKVIGTTTTD	765
Qy	755	-----	754
Db	766	ASGKYKFTDLNNGNYTVEFETPAGYTPTVKNNTADDKDSNGLTTTGVIKDADNM TLD RGF	825
Qy	755	-----TDENGKYQFDNL	766
		:	
Db	826	YKTPKYS LGDYVWYDSNKGDKQDSTEKG IKDVTVT LQNEKGEVIGTTKTDENGKYRFDNL	885

[illegible]

RESULT 14

ABJ18982

ID   ABJ18982 standard; protein; 1166 AA.

XX

AC ABJ18982;

XX

DT 06-MAR-2003 (first entry)

XX

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 153.

XX

KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

KW autoimmune disease; HIV; hepatitis.

XX

OS Staphylococcus sp.

XX

PN WO200259148-A2.

XX

PD 01-AUG-2002.

XX

PF 21-JAN-2002; 2002WO-EP000546.

XX

PR 26-JAN-2001; 2001AT-00000130.

XX

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX

PI Meinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;

PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;

PI Tempelmaier B;

XX

DR WPI; 2003-075410/07.

XX

PT Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or

PT preventing e.g. staphylococcal infections, comprises providing antibody

PT preparation.

XX

PS Example 7; Page 173; 252pp; English.

XX

Query Match 44.2%; Score 2131; DB 6; Length 1166;  
Best Local Similarity 40.8%; Pred. No. 1.1e-96;  
Matches 482; Conservative 148; Mismatches 266; Indels 286; Gaps 25;

Qy	7	LTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDSNMDEL	66
		:     : :   ::  :     :::   :   :         ::	
Db	10	ITKKGMI SNRLNKF SIRQYTVGTASILVGTTLIFGLGNQEAKAAENT--STENAKQDDAT	67
Qy	67	SDSNDQ--SSNEEKNDVINNS-----QSINTDDDNQIKKEETNSNDAIENRSKDITQST-	118
		:   :     :     :     :      :  : : : ::  :	
Db	68	TSDNKEVVSETENNSTTENNSTNPIKKETNTDSQPEAKKESTSS--STQKQQNNVTATTE	125
Qy	119	---TNVD-ENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASI	174
		:       : :      : : : : :  :  :  :	
Db	126	TKPQNIKENVKPSTDKTATEDTSVILEEKKAPNNTNNDVTTKPSSTSEPSTSEIQTKPTT	185
Qy	175	-QTSDNEENS RVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKIS	233
		:   :  : : :    : :     :	
Db	186	PQESTNIENSQPP-TPSKVDNQVTDATNP---KEPVNVSKEELKKNPEKLKELVRNDS	240
Qy	234	NQDELLNLPINEYENKVRPLSTTSAQPSSKRV-----TVNQLAAEQGSNVNHLIKVTDQ	287
		: : :  :           :	
Db	241	NTD-----HSTKPVATAPTSVAPKRVNAKMRFAVAQPAVASNNVNDLIKVTQK	289
Qy	288	SITEGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPK	347
		:      :     ::     : :      :      :	
Db	290	TIKVG-DGKDNVAAAHDGKDIEYDTEFTIDNKVKKGDTMTINYDKNVIPSDLTDKNDPID	348
Qy	348	IKDNSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVE	407
		:     :             : :                  : :	
Db	349	ITDPSGEVIAGKTFDKATKQITYTFTDYVDKYEDIKSRLTLYSYIDKKTVP-NETSLNLT	407
Qy	408	YKTALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTEVQTIYINPLRYSAKETNVN	467
		:    : : :      : : : :       :    :   :	
Db	408	FATAGKETSQNVTVDYQDPMVHGDSNIQSIFTKLEDEKQTIEQQIYVNPLKKSATNTKVD	467
Qy	468	ISGNG-----DEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTND-DYA	517
		: :       :        :          : :        :	
Db	468	IAGSOVDDYGNIKLGNGSTIIDONTEIKVYKVNSDOOLPOSNRIYDFSQYEDVTSQFDNK	527

[illegible]

RESULT 15

ABU42327

ID ABU42327 standard; protein; 1141 AA.

XX

AC ABU42327;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #27854.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS      Staphylococcus aureus.

XX

PN WO200277183-A2.



XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA46197.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 70251; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1141 AA;

Query Match 44.1%; Score 2127.5; DB 6; Length 1141;  
 Best Local Similarity 41.8%; Pred. No. 1.6e-96;

Matches 484; Conservative 150; Mismatches 260; Indels 265; Gaps 28;

Qy	7	LTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDSNMDEL	66
		:    : :  :  :     :  :   :         : :	
Db	10	ITKKGMI SNRLNKFSIRKYTVGTASILVGTTLIFGLGNQEAKAAENT--STENAKQDDAT	67
Qy	67	SDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTNVDENEA	126
		:   : :  :     :             :  : :	
Db	68	TSDNKEVVSETE---NNSTTEN-DSTNPIKK-ETNTDSQPEAKEESTTSSTQQQQNNVT	121
Qy	127	TFLQKTPQDNTQLKEEVVK---EPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNEENS	183
		:   : :       : :  :  :  :  :  :  :  :  :	
Db	122	ATTETKPQN---IEKENVKPSTDKTATEDTSVILEEKKAPNYT--NNDVTTKPSTSEIQT	176
Qy	184	RVSDFANSKIIESNTESNKEENTIEQPNKVREDS-IT--SQPSSYKNID-EKISNQDELL	239
		: : :        :  :  :  :  :  :  :  :  :	
Db	177	KPT-----TPQESTNIENSQPQTPSKVDNQVTDATNPKEPVNVSKEELKNNPEKL	227
Qy	240	NLPI---NEYENKVRPLST--TSAQP-----SSKRVTVNQLAAEQGSNVNHLIKVTDQSIT	290
		:   : :  :       :         :            :	
Db	228	KELVRNDNNTDRSTKPVATAPTSPAPKRLNAKMRFAVAQPAAVASNNVNDLITVTKQTIK	287
Qy	291	EGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKD	350
		:     :  :  :  :  :  :  :  :  :  :	
Db	288	VG-DGKDNVAAAHGDKDIEYDTEFTIDNKVKKGD TMTINYDKNVIPSDLTDKNDPIDITD	346
Qy	351	NSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKT	410
		:      :                :              :  :	
Db	347	PSGEVIAGKTFDKATKQITYTFTDYVDKYEDIKARLTLYSYIDKQAVP-NETSLNLT FAT	405
Qy	411	ALSSVNKTITVEYQKPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISG	470
		: :  :    : :  :  :  :  :  :  :  :  :  :	
Db	406	AGKETSQNVSVDYQDPMVHGDSNIQSI FTKL DENKQTIEQQIYVNPLKKTATNTKVDIAG	465
Qy	471	NG-----DEGSTIIDSTIIKVYKVGDNQNLPSNRIYDYSEYEDVTND-DYAQLG	520
		:       :                 :  :  :  :  :	
Db	466	SQVDDYGNIKLNGSGSTIIDQNT EIKVYKVNPNQQLPQSNRIYDFSQYEDVTSQFDNKKSF	525
Qy	521	NNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIQQTVMQTTINEYTGEFRTASYDNTI	580
		:   :  :  :  :            :  :  :  :  :  :	
Db	526	SNNVATLDFGDINSAYIIKVVS KYTPTSDGELDIAQGTSMRTT-DKY-GYNYAGYSNFI	583
Qy	581	AFSTSSGQGQDL-PPEKTYKIGDYVWEDVDKDG IQNTNDNEKPLSNVLVTLTPDGTSK	639
		:      :                :  :  :  :  :  :	
Db	584	VTSNDTGGGDGTVKPEEKLYKIGDYVWEDVDKDG VQGTDSKEKPMANVLVTLTPDGTTK	643
Qy	640	SVRTDEEGKYQFDGLKNGLTYKITFETPEGYTPTLKHSGTNPALDSEGNSVWVTINGQDD	699
		:     :     :          :   :     :  :  :	
Db	644	SVRTDANGHYEFGGLKDGETYTVKFETPAGYLP TKVNGTTDGEKDSNGSSITVKINGKDD	703
Qy	700	-----	699
Db	704	MSLDTGFYKEPKYNLGDYVWEDTNKDGIQDANE PGIKDVKVT LKDSTGKVIGTTT TDASG	763
Qy	700	-----MTIDSGFYQT	709
		:     :	
Db	764	KYKFTDL DNGNYTVEFETPAGYTPTVKNTTAEDKDSNGLTTTGVIKADNMTLDSGFYKT	823
Qy	710	PKYSLGNYVWYDTNKGDIQGDDEKGISGVKVLKDENGNIISTTTT DENGKYQFDNLNSG	769
		:     :                 :    :          :     :	
Db	824	PKYSLGDYVWYDSNKGDKQDSTEKG IKDVKVTLLNEKGEVIGTTKTDENGKYRFDNLDSG	883

Qy	770	NYIVHFDKPSGMTQTTTTDSGDDDEQDADGEEVHVITITDHDDFSIDNGYY-----	818
		: :: :    :: :    :                :   :	
Db	884	KYKVIFEKPAGLTQTVTNNTTEDD-KDADGGEVDVTITDHDDFILDNGYFEEDTSDS SDS	942
Qy	819	-----	818
Db	943	DS	1002
Qy	819	-----DDDSDSDSDSDSDSDSD-DSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDS	867
Db	1003	DS	1062
Qy	868	DSDSDSDSDSGLDNSSDKN-----TKD-----KLPTGANEDHDSKGTLLGA	909
		:     :        :    : :	
Db	1063	DSDSDSDSDSDSDSDSDSDSDAGKHTPVKPMSTTKDHHNKAKALPETGSENNGSNNATLFGG	1122
Qy	910	LFAGLGALLL-GKRRKNRK	927
		:      : :	
Db	1123	LFAALGSLLLFGRRKKQNK	1141

Search completed: June 20, 2006, 19:25:37  
Job time : 210 secs

SCORE 1.3    BuildDate: 12/06/2005